Report

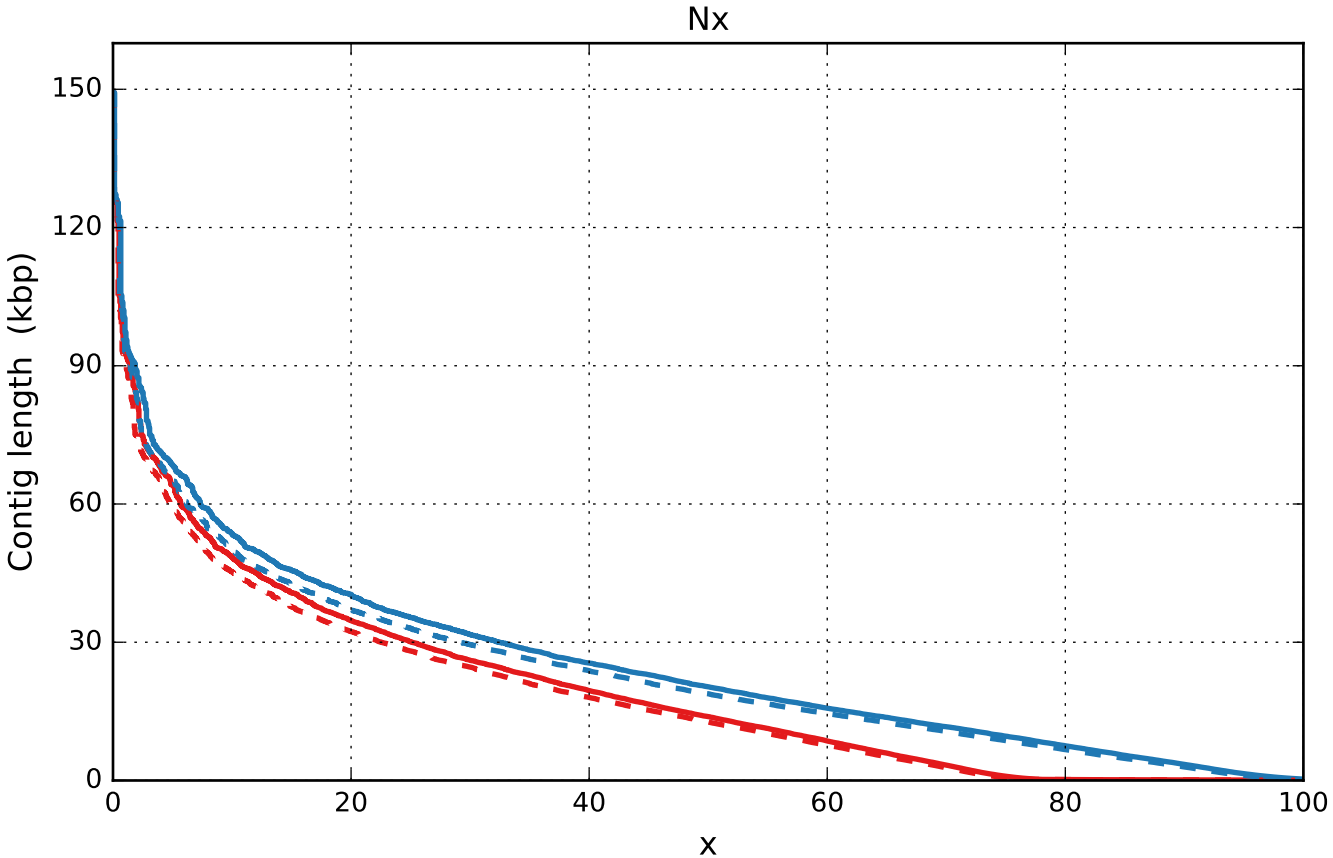
	mir159_multikmer.scafSeq	scaffolds_mir159_multikmer_300bp	mir159_multikmer.scafSeq broken	scaffolds_mir159_multikmer_300bp broken
# contigs (>= 0 bp)	287909	18267	293962	24320
# contigs (>= 1000 bp)	10737	10737	10966	10966
# contigs (>= 5000 bp)	5636	5636	5733	5733
# contigs (>= 10000 bp)	3646	3646	3632	3632
# contigs (>= 25000 bp)	1221	1221	1149	1149
# contigs (>= 50000 bp)	210	210	177	177
Total length (>= 0 bp)	151871645	117607777	151542929	117279061
Total length (>= 1000 bp)	113538632	113538632	111727104	111727104
Total length (>= 5000 bp)	101355878	101355878	98999047	98999047
Total length (>= 10000 bp)	87002244	87002244	83876142	83876142
Total length (>= 25000 bp)	48249496	48249496	44384722	44384722
Total length (>= 50000 bp)	13949494	13949494	11730559	11730559
# contigs	287909	18267	293962	24320
Largest contig	149281	149281	149281	149281
Total length	151871645	117607777	151542929	117279061
Reference length	119667750	119667750	119667750	119667750
GC (%)	37.10	36.01	37.10	36.01
Reference GC (%)	36.06	36.06	36.06	36.06
N50	13865	20323	12715	18820
NG50	19924	19924	18291	18291
N75	919	9607	618	8655
NG75	9106	9106	8015	8015
L50	2712	1690	2916	1808
LG50	1741	1741	1873	1873
L75	11119	3769	13428	4071
LG75	3934	3934	4287	4287
# misassemblies	783	577	535	329
# misassembled contigs	701	495	516	310
Misassembled contigs length	3641097	3605819	2138604	2103326
# local misassemblies	3018	2934	2630	2546
# scaffold gap size misassemblies	3945	3945	-	-
# unaligned contigs	117580 + 5312 part	831 + 782 part	118266 + 5222 part	1517 + 692 part
Unaligned length	14272496	875063	14242230	844797
Genome fraction (%)	97.540	95.948	97.603	96.002
Duplication ratio	1.179	1.017	1.176	1.014
# N's per 100 kbp	222.18	286.91	5.75	7.43
# mismatches per 100 kbp	19.03	16.98	16.98	14.70
# indels per 100 kbp	6.82	6.73	6.17	6.04
# genes	26090 + 2525 part	26040 + 2441 part	25081 + 3442 part	25015 + 3352 part
Largest alignment	149263	149263	149263	149263
NA50	13285	19674	12275	18248
NGA50	19219	19219	17839	17839
NA75	521	9102	417	8207
NGA75	8519	8519	7667	7667
LA50	2800	1738	2991	1851
LGA50	1791	1791	1917	1917
LA75	13399	3909	15783	4192
LGA75	4084	4084	4418	4418

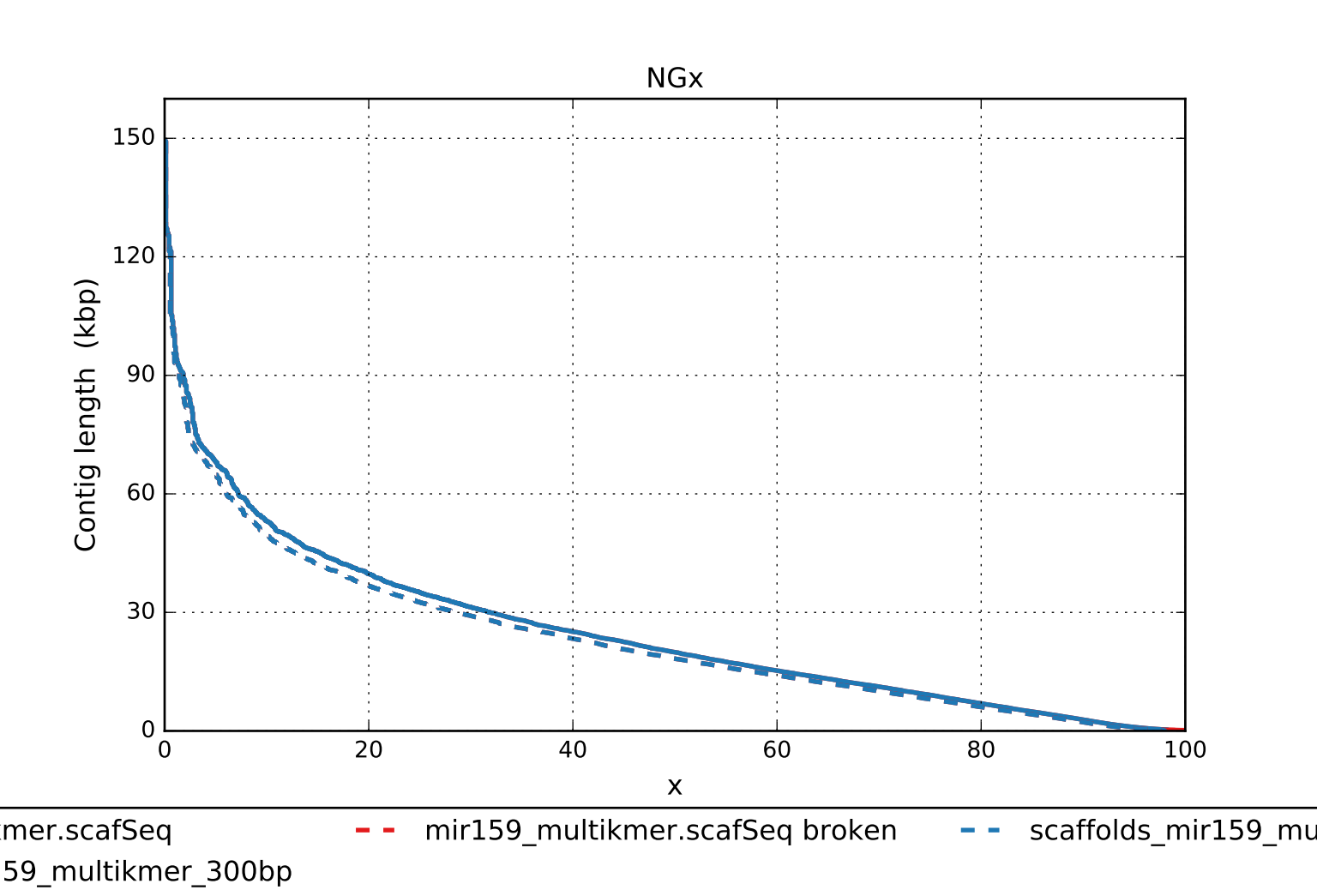
Misassemblies report

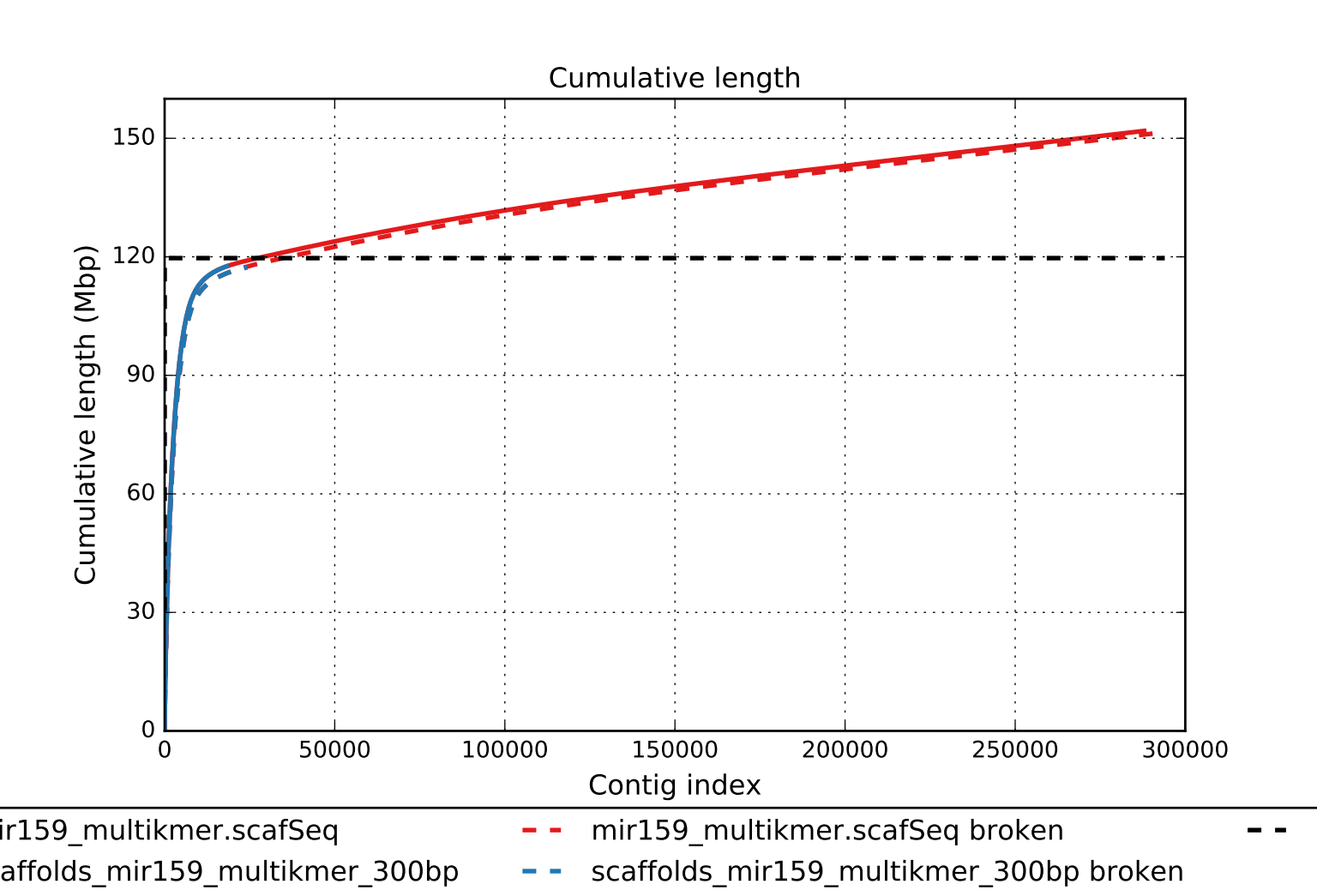
	mir159_multikmer.scafSeq	scaffolds_mir159_multikmer_300bp	mir159_multikmer.scafSeq broken	scaffolds_mir159_multikmer_300bp broken
# misassemblies	783	577	535	329
# relocations	295	244	190	139
# translocations	467	331	324	188
# inversions	21	2	21	2
# misassembled contigs	701	495	516	310
Misassembled contigs length	3641097	3605819	2138604	2103326
# local misassemblies	3018	2934	2630	2546
# scaffold gap size misassemblies	3945	3945	-	-
# mismatches	22211	19491	19831	16888
# indels	7959	7723	7205	6935
# short indels	5749	5536	5493	5248
# long indels	2210	2187	1712	1687
Indels length	82373	80705	68063	66317

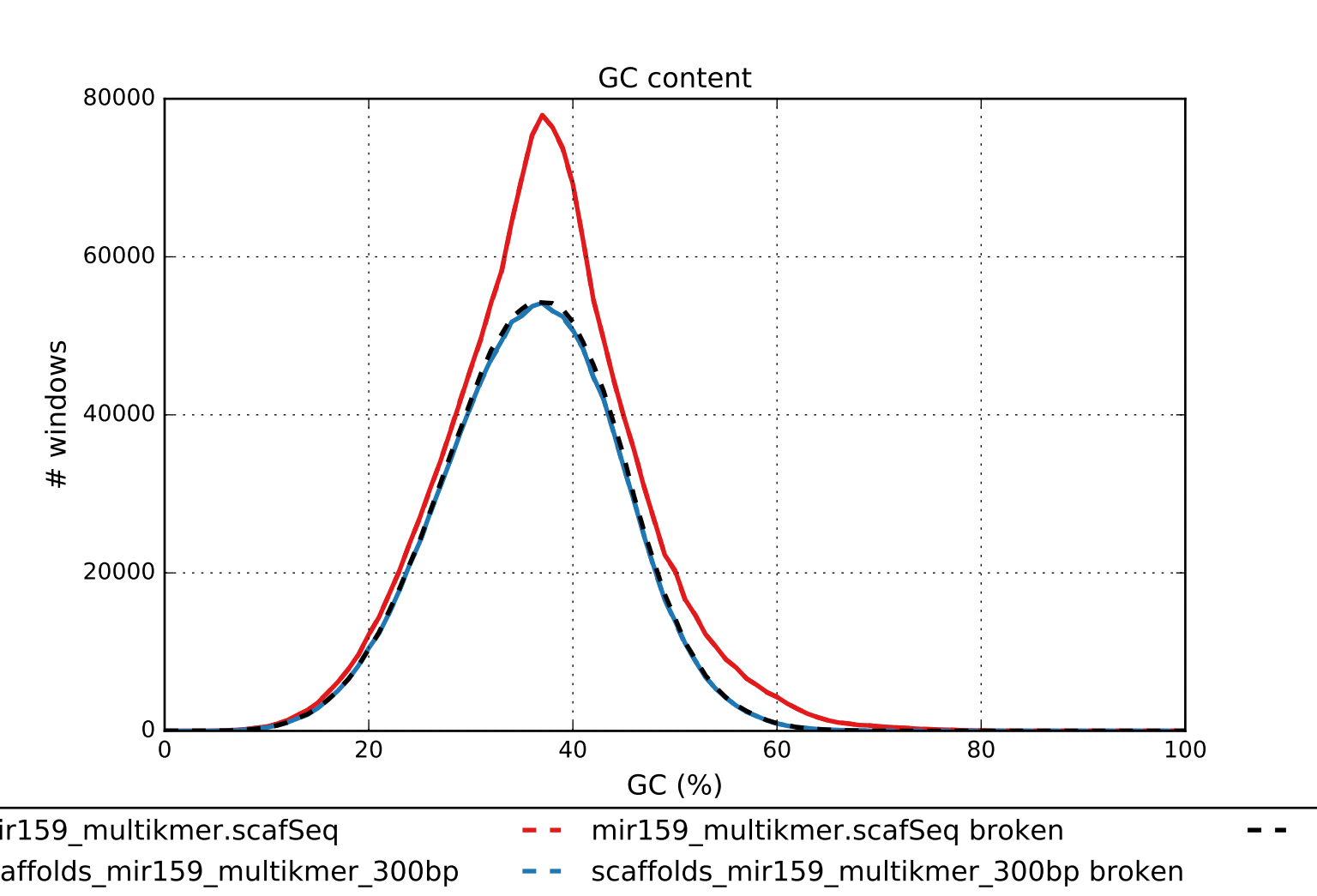
Unaligned report

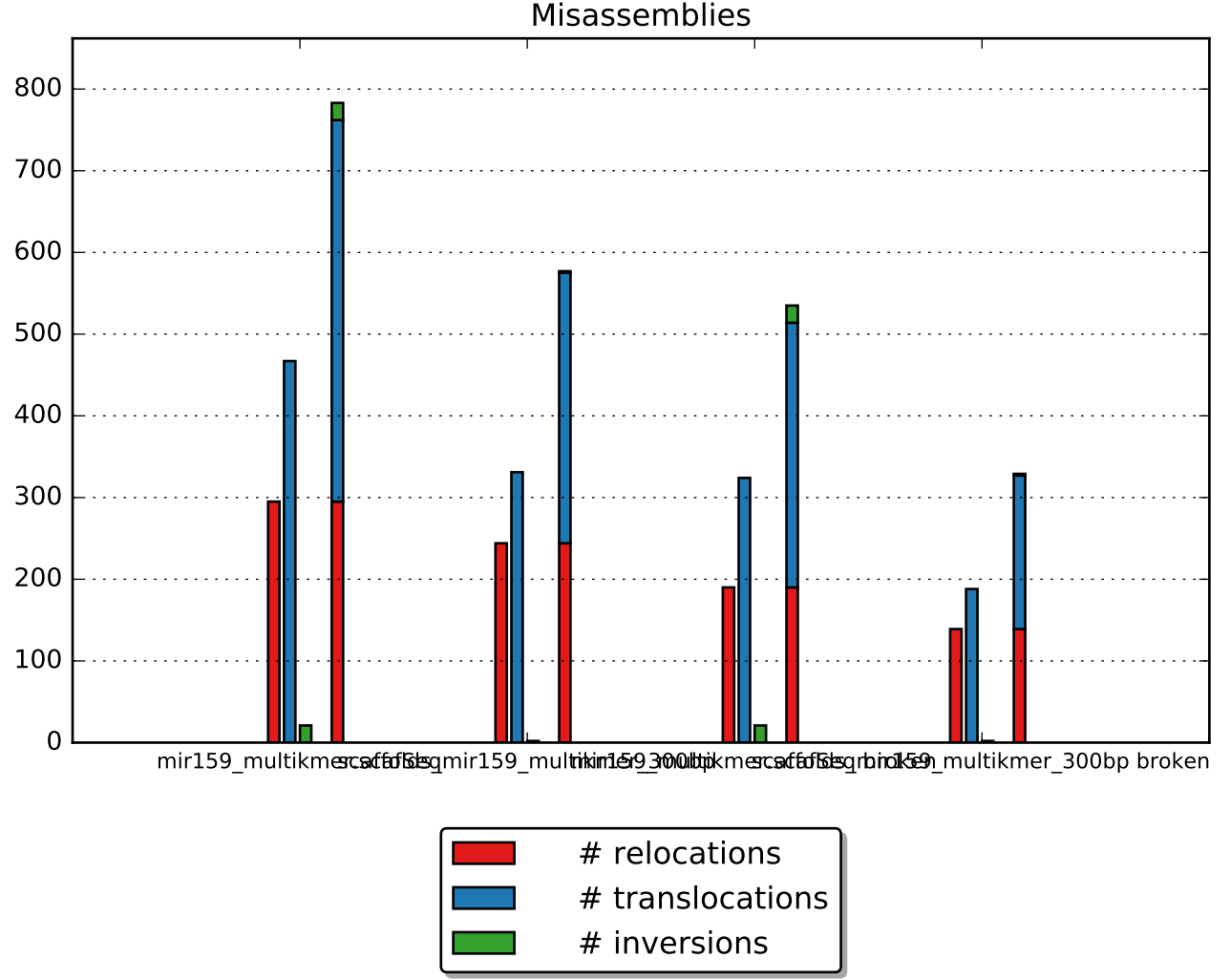
	mir159_multikmer.scafSeq	scaffolds_mir159_multikmer_300bp	mir159_multikmer.scafSeq broken	scaffolds_mir159_multikmer_300bp broken
# fully unaligned contigs	117580	831	118266	1517
Fully unaligned length	13750166	492057	13855610	597501
# partially unaligned contigs	5312	782	5222	692
# with misassembly	121	121	36	36
# both parts are significant	53	53	29	29
Partially unaligned length	522330	383006	386620	247296
# N's	337433	337425	8717	8709

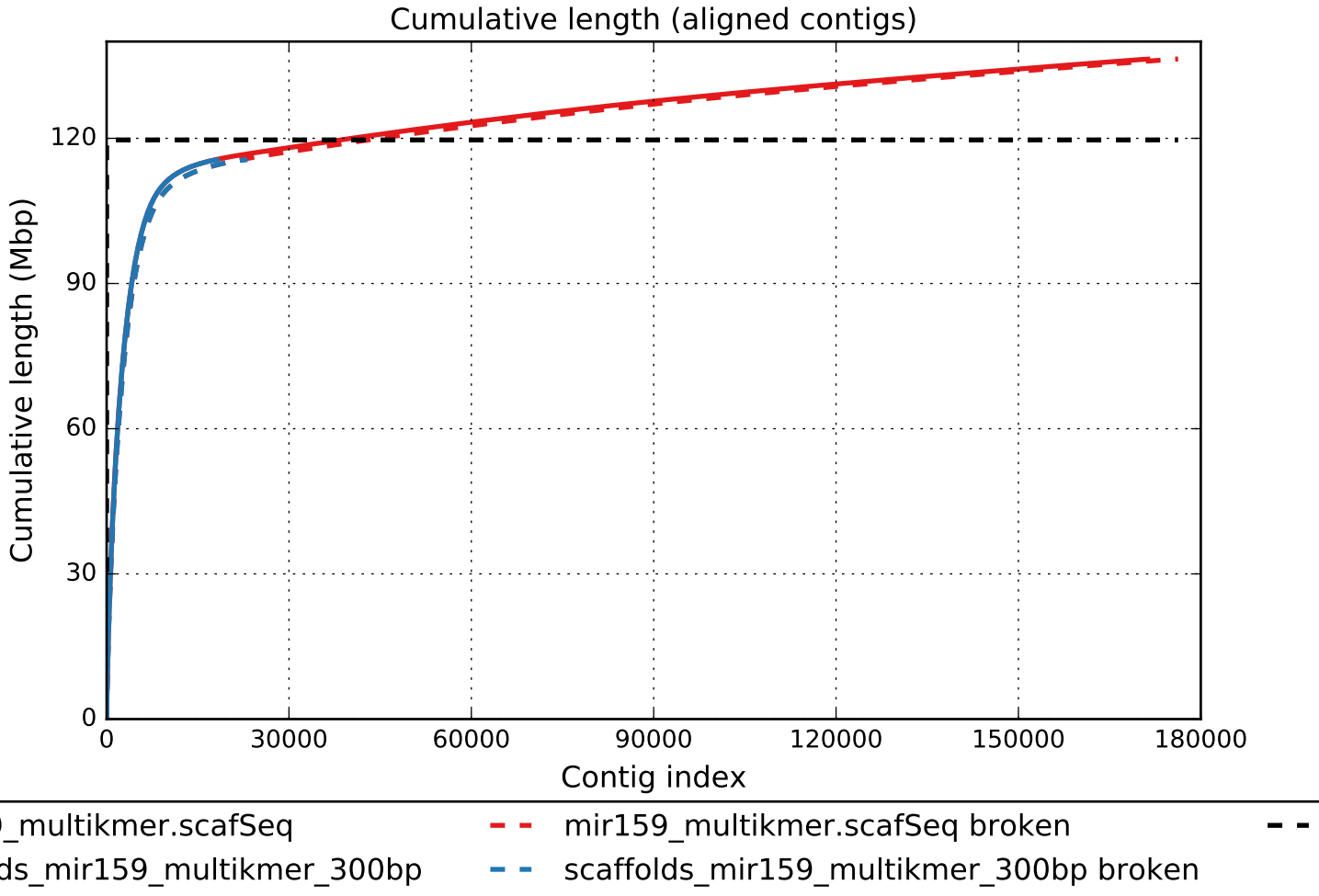

Nx
Contig length (kbp)
150
120
90
60
30
0
0
20
40
60
80
100
x
kmer.scafSeq
mir159_multikmer.scafSeq broken
scaffolds_mir159_mu
59_multikmer_300bp

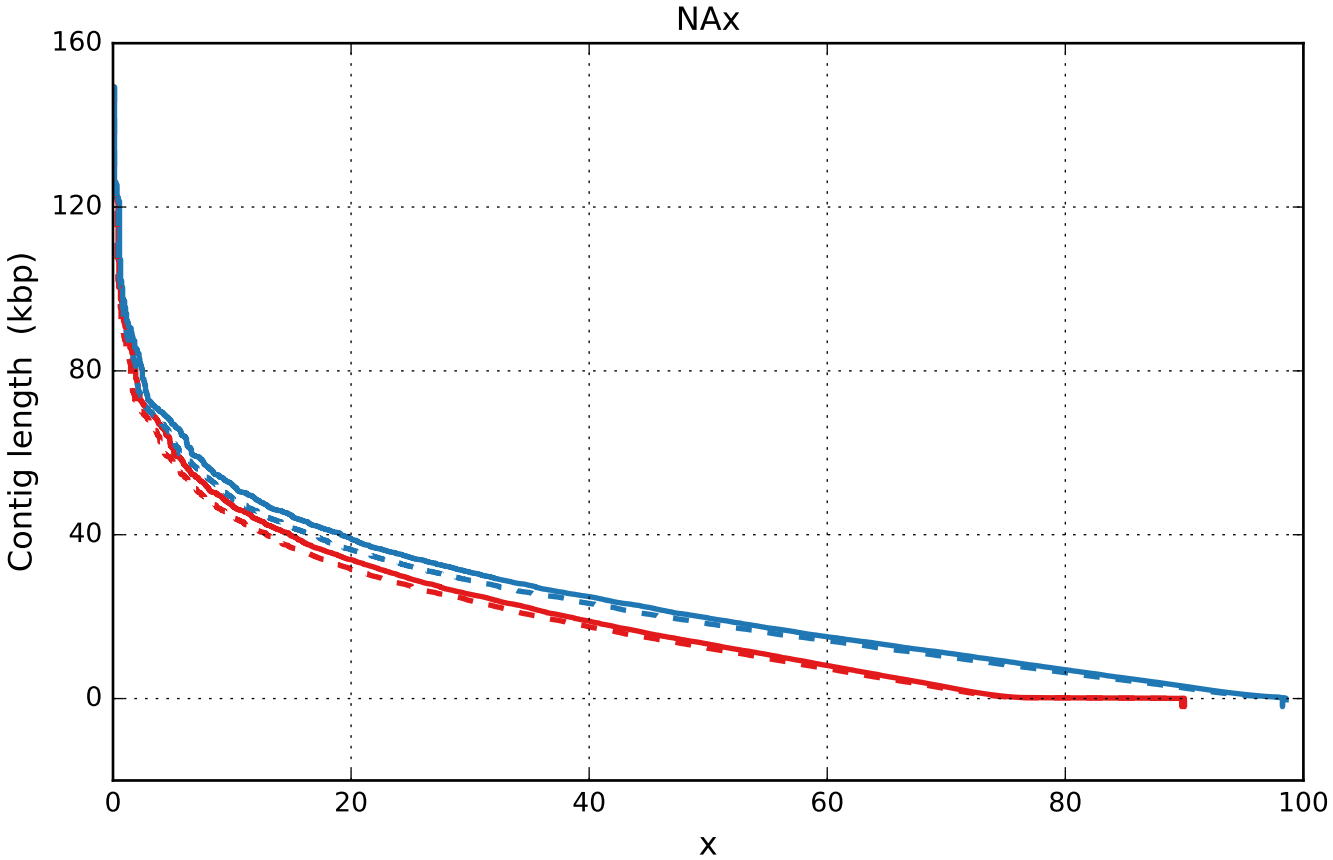

NGx
Contig length (kbp)
150
120
90
60
30
0
0
20
40
60
80
100
x
kmer.scafSeq
mir159_multikmer.scafSeq broken
scaffolds_mir159_mu
59_multikmer_300bp

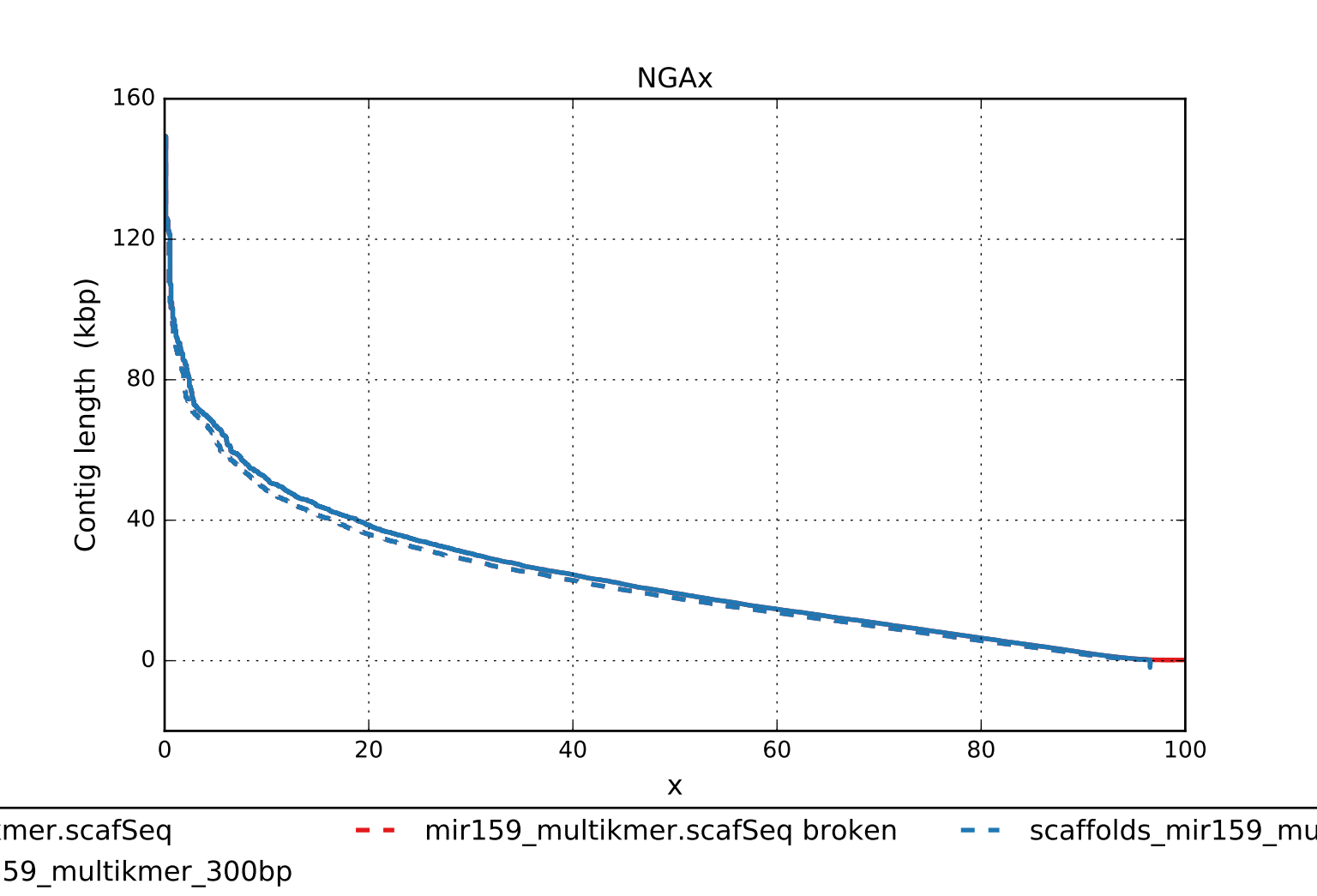

Cumulative length
Cumulative length (Mbp)
150
120
90
60
30
0
0
50000
100000
150000
200000
250000
300000
Contig index
ir159_multikmer.scafSeq
mir159_multikmer.scafSeq broken
affolds_mir159_multikmer_300bp
scaffolds_mir159_multikmer_300bp broken

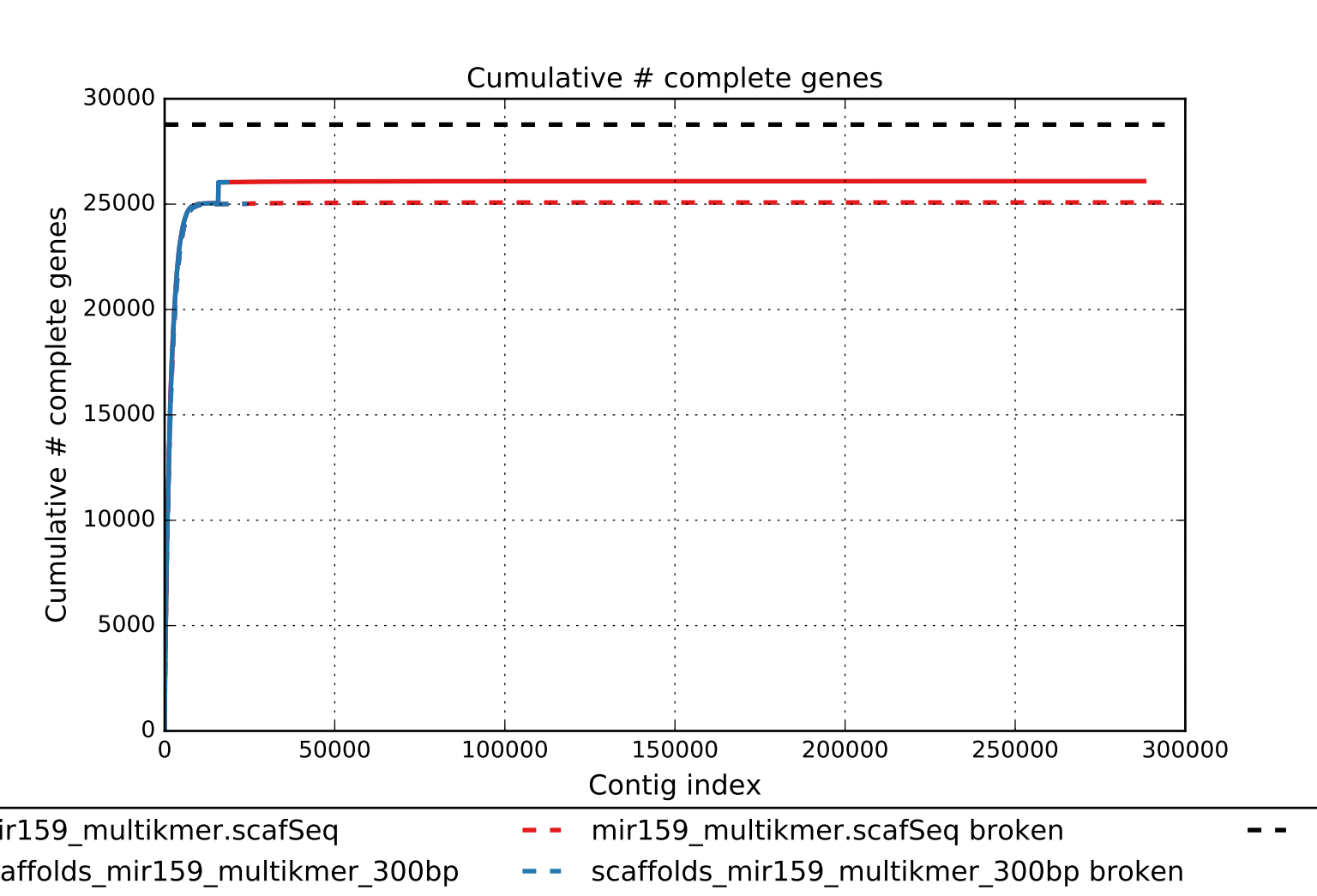

GC content
80000
60000
40000
20000
0
windows
0
20
40
60
80
100
GC (%)
ir159_multikmer.scafSeq
mir159_multikmer.scafSeq broken
affolds_mir159_multikmer_300bp
scaffolds_mir159_multikmer_300bp broken

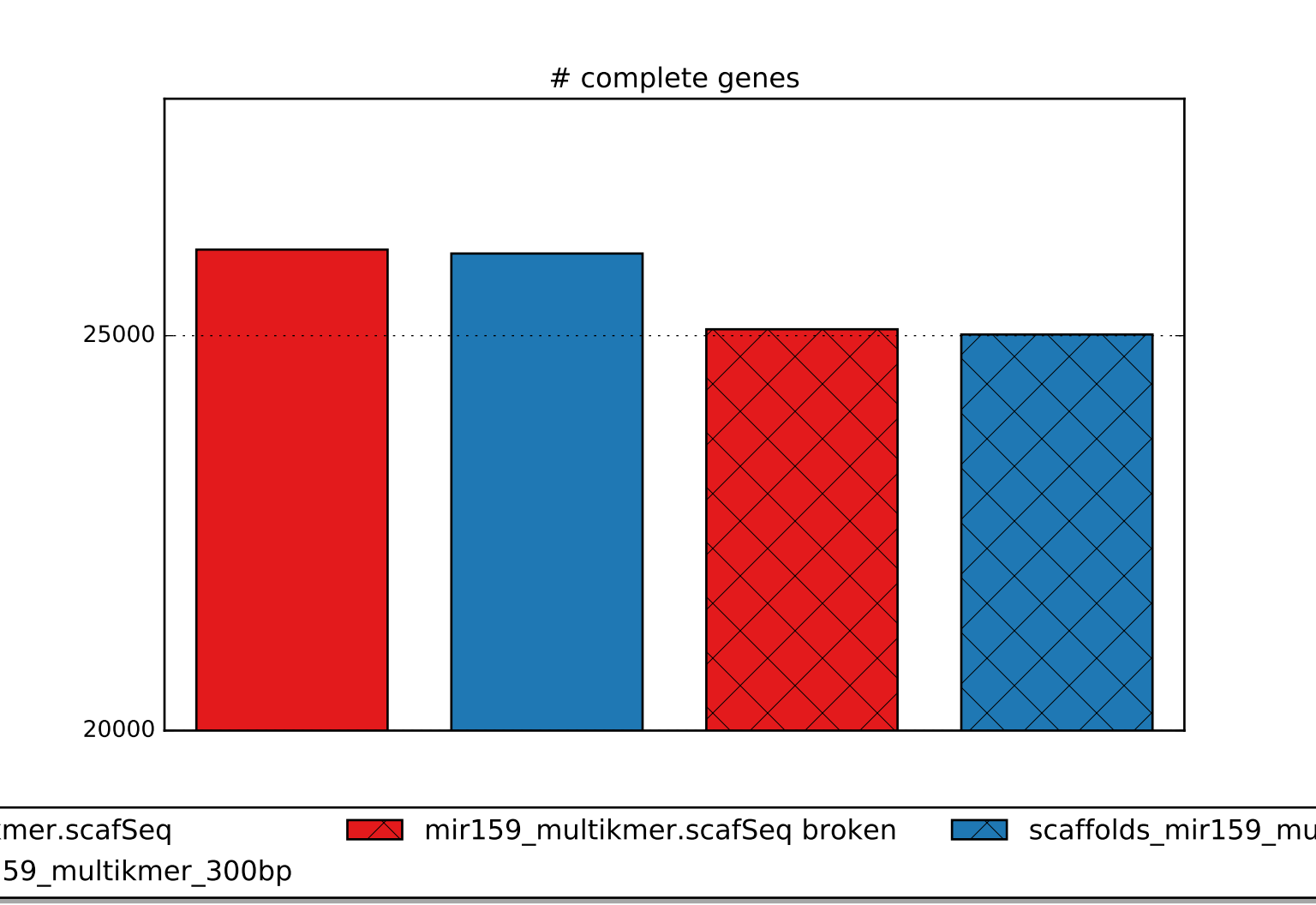

Misassemblies
800
700
600
500
400
300
200
100
0
mir159_multikmer_300bp broken
relocations
translocations
inversions

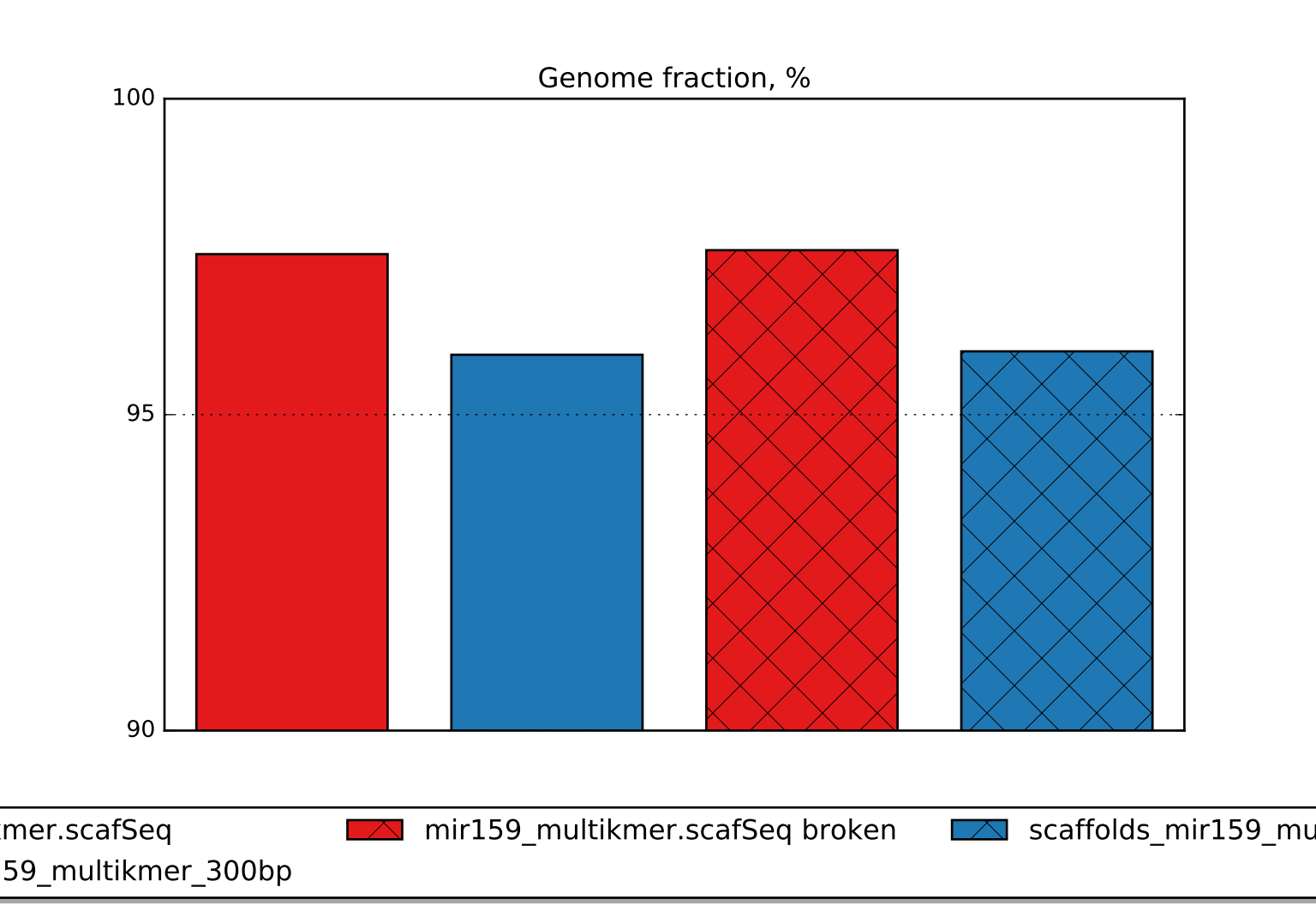

Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
30
60
90
120
0
30000
60000
90000
120000
150000
180000
Contig index
ir159_multikmer.scafSeq
mir159_multikmer.scafSeq broken
affolds_mir159_multikmer_300bp
scaffolds_mir159_multikmer_300bp broken


NAx
160
120
80
40
0
Contig length (kbp)
0
20
40
60
80
100
x
kmer.scafSeq
mir159_multikmer.scafSeq broken
scaffolds_mir159_mu
59_multikmer_300bp


NGAx
160
120
80
40
0
Contig length (kbp)
0
20
40
60
80
100
x
kmer.scafSeq
mir159_multikmer.scafSeq broken
scaffolds_mir159_mu
59_multikmer_300bp


Cumulative # complete genes
30000
25000
20000
15000
10000
5000
0
Cumulative # complete genes
0
50000
100000
150000
200000
250000
300000
Contig index
ir159_multikmer.scafSeq
mir159_multikmer.scafSeq broken
affolds_mir159_multikmer_300bp
scaffolds_mir159_multikmer_300bp broken


complete genes
25000
20000
kmer.scafSeq
mir159_multikmer.scafSeq broken
scaffolds_mir159_mu
59_multikmer_300bp


Genome fraction, %
100
95
90
kmer.scafSeq
mir159_multikmer.scafSeq broken
scaffolds_mir159_mu
59_multikmer_300bp